


**This Page Is Inserted by IFW Operations
and is not a part of the Official Record**

BEST AVAILABLE IMAGES

**Defective images within this document are accurate representation of
The original documents submitted by the applicant.**

Defects in the images may include (but are not limited to):

- **BLACK BORDERS**
- **TEXT CUT OFF AT TOP, BOTTOM OR SIDES**
- **FADED TEXT**
- **ILLEGIBLE TEXT**
-  **SKEWED/SLANTED IMAGES**
- **COLORED PHOTOS**
- **BLACK OR VERY BLACK AND WHITE DARK PHOTOS**
- **GRAY SCALE DOCUMENTS**

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 23:00:18 ; Search time 1096 Seconds
(without alignments)
557.627 Million cell updates/sec

Title: US-09-723-326B-1
Perfect score: 21
Sequence: 1 tgcacgtctcgcacgacgta 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Search: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBankl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_pln: *
35: em_hcg_rnd: *
36: em_hcg_mam: *
37: em_hcg_vrl: *
38: em_sy: *
39: em_hgtgo_hum: *
40: em_hgtgo_mus: *
41: em_hgtgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	6	AX189770 Sequence
2	21	100.0	43	6	AX189774 Sequence
3	21	100.0	86	6	AX189775 Sequence
4	21	100.0	129	6	AX189778 Sequence
5	20	95.2	24	6	AX147416 Sequence
6	19	90.5	19	6	AX147421 Sequence
7	19	90.5	24	6	AX6287 Sequence 2
8	19	90.5	24	6	AX023673 Sequence
9	19	90.5	24	6	AX048713 Sequence
10	19	90.5	24	6	AX147415 Sequence
11	19	90.5	41	6	AR073928 Sequence
12	19	90.5	123	6	AX189776 Sequence
13	19	90.5	229	6	AX023662 Sequence
14	19	90.5	366	5	AX353996 Sequence
15	19	90.5	513	6	AX150246 Sequence
16	19	90.5	1110	10	MUSPCK1
17	19	90.5	1943	10	MMPGKSR
18	19	90.5	3297	12	AF090453
19	19	90.5	3426	12	AF090454
20	19	90.5	4699	12	AF346623
21	19	90.5	4768	6	AX299821
22	19	90.5	4768	6	AX352704
23	19	90.5	4847	6	AX191674
24	19	90.5	5365	6	AX114854
25	19	90.5	5482	12	AF090455
26	19	90.5	5505	2	AL831717
27	19	90.5	5568	12	AF335419
28	19	90.5	5568	12	AF335420
29	19	90.5	5608	12	AF092169
30	19	90.5	5608	12	AF092172
31	19	90.5	5608	12	AF092173
32	19	90.5	5608	12	AF092174
33	19	90.5	5608	12	AF092541
34	19	90.5	5608	12	AF092542
35	19	90.5	5608	12	AF092543
36	19	90.5	5608	12	AF092567
37	19	90.5	5830	12	AY028413
38	19	90.5	5842	12	AY028415
39	19	90.5	6293	12	AF397196
40	19	90.5	6355	6	AX299822
41	19	90.5	6355	6	AX352705
42	19	90.5	7090	6	AX150263
43	19	90.5	8157	2	AL831743
44	19	90.5	8387	6	AR070490
45	19	90.5	8388	6	ARI79512

ALIGNMENTS

RESULT 1
AX189770
LOCUS
DEFINITION Sequence 1 from Patent WO0148187.
ACCESSION AX189770
VERSION AX189770.1 GI:15143141
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 21)
AUTHORS Webster, K.A.
TITLE A molecular switch for regulating mammalian gene expression
JOURNAL Patent: WO 0148187-A 1 05-JUL-2001;
The University of Miami (US)

FEATURES
source
Location/Qualifiers
1. .21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
BASE COUNT 4 a 5 g 5 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACGTCCTGCACGACGTA 21
|||||
Db 1 TGTACGTCCTGCACGACGTA 21

RESULT 2
AXI89774 43 bp DNA Linear PAT 08-AUG-2001
LOCUS AXI89774
DEFINITION Sequence 5 from Patent W00148187.
ACCESSION AXI89774
VERSION AXI89774.1 GI:15143145
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 43)
AUTHORS Webster,K.A.
TITLE A molecular switch for regulating mammalian gene expression
JOURNAL Patent: WO 0148187-A 5 05-JUL-2001;
The University of Miami (US)
Location/Qualifiers
1. .43
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
BASE COUNT 8 a 16 c 11 g 8 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACGTCCTGCACGACGTA 21
|||||
Db 23 TGTACGTCCTGCACGACGTA 43

RESULT 3
AXI89775 86 bp DNA Linear PAT 08-AUG-2001
LOCUS AXI89775
DEFINITION Sequence 6 from Patent W00148187.
ACCESSION AXI89775
VERSION AXI89775.1 GI:15143146
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 86)
AUTHORS Webster,K.A.
TITLE A molecular switch for regulating mammalian gene expression
JOURNAL Patent: WO 0148187-A 6 05-JUL-2001;
The University of Miami (US)
Location/Qualifiers
1. .86
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
BASE COUNT 16 a 32 c 22 g 16 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 86;

Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACGTCCTGCACGACGTA 21
|||||
Db 23 TGTACGTCCTGCACGACGTA 43

RESULT 4
AXI89778 129 bp DNA Linear PAT 08-AUG-2001
LOCUS AXI89778
DEFINITION Sequence 9 from Patent W00148187.
ACCESSION AXI89778
VERSION AXI89778.1 GI:15143149
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 129)
AUTHORS Webster,K.A.
TITLE A molecular switch for regulating mammalian gene expression
JOURNAL Patent: WO 0148187-A 9 05-JUL-2001;
The University of Miami (US)
Location/Qualifiers
1. .129
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
BASE COUNT 24 a 48 c 27 g 30 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACGTCCTGCACGACGTA 21
|||||
Db 23 TGTACGTCCTGCACGACGTA 43

RESULT 5
AXI47416/c 24 bp DNA Linear PAT 08-JUN-2001
LOCUS AXI47416
DEFINITION Sequence 4 from Patent W00136616.
ACCESSION AXI47416
VERSION AXI47416.1 GI:14346573
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Beuzard,Y., Payen,E., Scherman,D. and Bellen,M.
TITLE Acid nucleic construct bearing a system regulating the expression
JOURNAL Institut NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
(FR) : Aventis Pharma S.A. (FR)
Location/Qualifiers
1. .24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="HRE2"
BASE COUNT 5 a 7 c 8 g 4 t
ORIGIN

Query Match 95.2%; Score 20; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACGTCCTGCACGACGTA 20
|||||
Db 23 TGTACGTCCTGCACGACGTA 4

RESULT 6
AX147421/c
LOCUS AX147421 19 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 9 from Patent WO0136616.
ACCESSION AX147421
VERSION AX147421.1 GI:14346578
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
1 (bases 1 to 19)
REFERENCE
AUTHORS Beuzaud,Y., Payen,E., Scherman,D. and Beltan,M.
TITLE Acid nucleic construct bearing a system regulating the expression of a gene
JOURNAL
PATENT: WO 0136616-A 9 25-MAY-2001;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR) ; Aventis Pharma S.A. (FR)
FEATURES
source
Location/Qualifiers
1..19
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="HRE"
BASE COUNT 4 a 5 c 7 g 3 t
ORIGIN
Query Match 90.5%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTACGTCCTGCACGACG 19
|||||
DB 19 TGTACGTCCTGCACGACG 1

RESULT 7
A46287/c
LOCUS A46287 24 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 2 from Patent WO9521927.
ACCESSION A46287
VERSION A46287.1 GI:2300513
KEYWORDS
SOURCE
ORGANISM
unidentified.
unidentified.
unclassified.
1 (bases 1 to 24)
REFERENCE
AUTHORS Ratcliffe,P.J., Firth,J.D., Harris,A.L. and Pugh,C.W.
TITLE TARGETING GENE THERAPY
JOURNAL
PATENT: WO 9521927-A 2 17-AUG-1995;
ISIS INNOVATION (GB)
FEATURES
source
Location/Qualifiers
1..24
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN
Query Match 90.5%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTACGTCCTGCACGACG 19
|||||
DB 21 TGTACGTCCTGCACGACG 3

RESULT 8
AX023673/c
LOCUS AX023673 24 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 15 from Patent WO0017371.
ACCESSION AX023673
VERSION AX023673.1 GI:10184034
KEYWORDS

SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Binley,K.W. and Naylor,S.
TITLE Polynucleotide constructs and uses thereof
JOURNAL
PATENT: WO 0017371-A 15 30-MAR-2000;
BINLEY KATIE MARY (GB) ; NAYLOR STUART (GB) ; OXFORD BIOMEDICA LTD (GB)
FEATURES
source
Location/Qualifiers
1..24
/organism="Mus sp."
/db_xref="taxon:10095"
BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN
Query Match 90.5%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTACGTCCTGCACGACG 19
|||||
DB 21 TGTACGTCCTGCACGACG 3

RESULT 9
AX048713/c
LOCUS AX048713 24 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 13 from Patent WO0069908.
ACCESSION AX048713
VERSION AX048713.1 GI:12225858
KEYWORDS
SOURCE
ORGANISM
Mus sp.
Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Ratcliffe,P.J., Maxwell,P.H. and Pugh,C.W.
TITLE Interaction between the vhl tumour suppressor and hypoxia inducible factor; and assay methods relating thereto
JOURNAL
PATENT: WO 0069908-A 13 23-NOV-2000;
ISIS INNOVATION LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..24
/organism="Mus sp."
/db_xref="taxon:10095"
BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN
Query Match 90.5%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTACGTCCTGCACGACG 19
|||||
DB 21 TGTACGTCCTGCACGACG 3

RESULT 10
AX147415
LOCUS AX147415 24 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 3 from Patent WO0136616.
ACCESSION AX147415
VERSION AX147415.1 GI:14346572
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.
1 (bases 1 to 24)
REFERENCE
AUTHORS Beuzaud,Y., Payen,E., Scherman,D. and Beltan,M.
TITLE Acid nucleic construct bearing a system regulating the expression of a gene

JOURNAL Patent: WO 0136616-A 3 25-MAY-2001;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
(FR) : Aventis Pharma S.A. (FR)
FEATURES location/Qualifiers
SOURCE 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="HRE1"

BASE COUNT 4 a 8 c 7 g 5 t
ORIGIN

Query Match 90.5%; Score 19; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTACGTCCTGCACGACG 19
|||||
Db 6 TGTACGTCCTGCACGACG 24

RESULT 11
LOCUS AR073928/c 41 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 2 from patent US 5952226.
ACCESSION AR073928
VERSION AR073928.1 GI:10000688
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Aebischer,P., Deglon,N., Regulier,E. and Rinsch,C.
TITLE Hypoxia responsive EPO producing cells
JOURNAL Patent: US 5952226-A 2 14-SEP-1999;
FEATURES location/Qualifiers
SOURCE 1..41
/organism="unknown"

BASE COUNT 8 a 11 c 15 g 7 t
ORIGIN

Query Match 90.5%; Score 19; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTACGTCCTGCACGACG 19
|||||
Db 41 TGTACGTCCTGCACGACG 23

RESULT 12
LOCUS AX189776 123 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from Patent WO0148187.
ACCESSION AX189776
VERSION AX189776.1 GI:15143147
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 123)
AUTHORS Webster,K.A.
TITLE A molecular switch for regulating mammalian gene expression
JOURNAL Patent: WO 0148187-A 7 05-JUL-2001;
FEATURES location/Qualifiers
SOURCE 1..123
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT 22 a 47 c 32 g 22 t
ORIGIN

Query Match 90.5%; Score 19; DB 6; Length 123;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTACGTCCTGCACGACG 19
|||||
Db 101 TGTACGTCCTGCACGACG 119

RESULT 13
LOCUS AX023662/c 229 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 4 from Patent WO0017371.
ACCESSION AX023662
VERSION AX023662.1 GI:10184023
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 229)
AUTHORS Binley,K.M. and Naylor,S.
TITLE Polynucleotide constructs and uses thereof
JOURNAL Patent: WO 0017371-A 4 30-MAR-2000;
BINLEY KATIE MARY (GB) ; NAYLOR STUART (GB) ; OXFORD BIOMEDICA LTD (GB)

FEATURES location/Qualifiers
SOURCE 1..229
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic construct"

BASE COUNT 52 a 68 c 55 g 54 t
ORIGIN

Query Match 90.5%; Score 19; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTACGTCCTGCACGACG 19
|||||
Db 30 TGTACGTCCTGCACGACG 12

RESULT 14
LOCUS AF353996/c 366 bp DNA linear VRT 08-MAY-2001
DEFINITION Cyprinus carpio pmtHGH-transgene flanking sequence.
ACCESSION AF353996
VERSION AF353996.1 GI:13991589
KEYWORDS
SOURCE Cyprinus carpio.
ORGANISM Cyprinus carpio.
REFERENCE 1 (bases 1 to 366)
AUTHORS Wu,B., Sun,Y., Wang,Y. and Zhu,Z.
TITLE Molecular polymorphic and sequences flanking pmtHGH-transgene in F4 transgenic common carp unpublished

JOURNAL 2 (bases 1 to 366)
AUTHORS Wu,B., Sun,Y., Wang,Y. and Zhu,Z.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2001) Fish Genetics & Breeding, Institute of Hydrobiology, Academia Sinica, Wujiangshan, Wuhan, Hubei 430072, P.R.China

FEATURES location/Qualifiers
SOURCE 1..366
/organism="Cyprinus carpio"
/db_xref="taxon:7962"
misc_feature 1..366
/note="pmtHGH-transgene flanking sequence; similar to Mus musculus phosphoglycerate kinase-1 gene exon 1"

BASE COUNT 64 a 120 c 106 g 76 t
ORIGIN

Query Match 90.5%; Score 19; DB 5; Length 366;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTACGTCCTGCACGACG 19
 ||||||||||||||||
 Db 236 TGTACGTCCTGCACGACG 218

RESULT 15
 AX150246/c 513 bp DNA linear PAT 08-JUN-2001
 LOCUS AX150246
 DEFINITION Sequence 1 from Patent WO0136615.
 ACCESSION AX150246
 VERSION AX150246.1 GI:14348266
 KEYWORDS

SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 513)
 TITLE Kochanek, S. and Schiedner, G.
 JOURNAL Permanent amniocyte cell line, the production thereof and its use
 for producing gene transfer vectors
 Patent: WO 0136615-A 1 25-MAY-2001;
 Kochanek, Stefan (DE)

FEATURES
 source location/qualifiers
 1..513
 /organism="Mus sp."
 /db_xref="taxon:10095"
 /note="Phosphoglycerat-Kinase-Promoter"
 BASE COUNT 79 a 171 c 161 g 102 t
 ORIGIN

Query Match 90.5%; Score 19; DB 6; Length 513;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTACGTCCTGCACGACG 19
 ||||||||||||||||
 Db 235 TGTACGTCCTGCACGACG 217

Search completed: July 9, 2003, 12:38:35
 Elapsed time : 1098 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 9, 2003, 09:54:41 ; Search time 145 Seconds
(without alignments)
326.151 Million cell updates/sec

Title: US-09-723-326B-1
Perfect score: 21
Sequence: 1 tttacgtctcgcacgacgta 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Search: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N.GeneSeq_101002.*
2: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1980.DAT.*
3: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1981.DAT.*
4: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1982.DAT.*
5: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1983.DAT.*
6: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1984.DAT.*
7: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1985.DAT.*
8: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1986.DAT.*
9: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1987.DAT.*
10: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1988.DAT.*
11: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1989.DAT.*
12: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1990.DAT.*
13: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1991.DAT.*
14: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1992.DAT.*
15: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1993.DAT.*
16: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1994.DAT.*
17: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1995.DAT.*
18: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1996.DAT.*
19: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1997.DAT.*
20: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1998.DAT.*
21: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA1999.DAT.*
22: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA2000.DAT.*
23: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA2001A.DAT.*
24: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA2001B.DAT.*
25: /SIDs2/gcgdata/geneSeq/geneSeqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	AAH42134	HRE element from t
2	21	100.0	43	AAH42138	Synapsin gene SIL
3	21	100.0	86	AAH42139	Synapsin gene SIL
4	21	100.0	129	AAH42142	Synapsin gene SIL
5	19	90.5	19	AAH42142	Nucleotide fragmen
6	19	90.5	24	AAH42142	Hypoxia-inducible
7	19	90.5	24	AAH42142	Hypoxia-inducible
8	19	90.5	24	AAH42142	Murine HRE mPKC DN
9	19	90.5	24	AAH42142	Murine hypoxic res

10	19	90.5	123	22	AAH42140	Synapsin gene SIL
11	19	90.5	229	20	AAH42139	PKC derived enhanc
12	19	90.5	229	21	AAH42139	Murine PKC HRE der
13	19	90.5	513	22	AAH20729	Murine phosphoglyc
14	19	90.5	4768	22	AAH42019	Plasmid vector pDG
15	19	90.5	4768	24	AAH42019	Nucleotide sequenc
16	19	90.5	4768	24	AAH42019	Plasmid pDG2 vecto
17	19	90.5	4768	24	AAH42019	Gene targeting ve
18	19	90.5	4847	22	AAH42019	PKC-cre PA vector
19	19	90.5	5365	22	AAH42019	Retroviral vector
20	19	90.5	5377	21	AAH42019	Expression vector
21	19	90.5	5581	22	AAH42019	Hprt gene containi
22	19	90.5	6355	22	AAH42019	Plasmid vector pDG
23	19	90.5	6355	24	AAH42019	Nucleotide sequenc
24	19	90.5	6355	24	AAH42019	Plasmid pDG4 vecto
25	19	90.5	6355	24	AAH42019	Gene targeting ve
26	19	90.5	7090	22	AAH42019	Plasmid pGEM-PCR
27	19	90.5	7617	18	AAH42019	Vector M48 used fo
28	19	90.5	8388	15	AAH42019	Expression vector
29	19	90.5	9725	21	AAH42019	Expression vector
30	19	90.5	9732	21	AAH42019	Expression vector
31	19	90.5	9738	21	AAH42019	Expression vector
32	19	90.5	9873	21	AAH42019	Expression vector
33	19	90.5	10054	21	AAH42019	Expression vector
34	19	90.5	11162	24	AAH42019	DNA of the gene ve
35	19	90.5	11162	24	AAH42019	Human TNK-TPA DNA
36	19	90.5	11162	24	AAH42019	Human mutant tLisu
37	19	90.5	11162	24	AAH42019	Gene vector sequen
38	19	90.5	13928	22	AAH42019	Haemophilus B gene
39	19	90.5	15692	20	AAH42019	London-PAD App tar
40	19	90.5	15692	20	AAH42019	Swedish/London-PAD
41	19	90.5	15701	20	AAH42019	Swedish-PAD App713
42	18	85.7	18	16	AAH42019	Hypoxia-inducible
43	18	85.7	18	21	AAH42019	Murine PKC1 derive
44	18	85.7	72	20	AAH42019	HRE-containing enh
45	18	85.7	72	21	AAH42019	Murine PKC HRE HIF

ALIGNMENTS

RESULT 1	AAH42134	standard; DNA; 21 BP.
ID	AAH42134	
AC	AAH42134	
XX	17-SEP-2001 (first entry)	
DT	HRE element from the human phosphoglycerate kinase gene.	
DE	Expression vector; silencer element; inducible element;	
KW	silencer-inducible region; gene therapy; cardiac disease;	
KW	immunodeficiency; allergy; anemia; thalassemia; autoimmune disease;	
KW	shock; hemophilia; inflammation; stress; ischemia; hypoxic condition;	
KW	carcinoma; leukemia; Hodgkin disease; Kaposi sarcoma;	
KW	hypoxia response enhancer; HRE; phosphoglycerate kinase gene; ss.	
OS	Homo sapiens.	
XX	WO200148187-A2.	
PN	05-JUL-2001.	
PD	15-DEC-2000; 2000WO-US33269.	
XX	23-DEC-1999; 99US-0171597.	
PR	28-NOV-2000; 2000US-0723326.	
XX	(UTM-) UNIV MIAMI.	
PA	Webster KA;	
XX		

DR WPI: 2001-441715/47.
XX
XX Novel isolated expression vector useful therapeutically, comprises
PT silencer elements and conditionally inducible elements to form
PT silencer-inducible region, and a promoter in operative linkage with the
PT region -
XX
XX Disclosure: Page 24; 49pp; English.
XX
XX The specification describes an expression vector. The vector comprises
CC silencer elements and conditionally inducible elements to form a
CC silencer-inducible region (IR), and a promoter in operative linkage
CC with IR, where the promoter is regulated by IR, and upstream of the
CC expressed region. The vector is useful diagnostically, therapeutically,
CC prophylactically to make models of human disease. It is useful in gene
CC therapy, production of recombinant biologicals, genetic diagnosis, drug
CC screening, and genetic research (e.g., genomics, proteomics, in vivo
CC and in vitro models of human disease). It is useful for treating cardiac
CC disease (by reduction or prevention of ischemic damage, inhibition of
CC restenosis, neutralization of other pathological effects of heart or
CC vascular disease, or diagnosis of hypoxia), acquired or inherited
CC immunodeficiency, allergy, anemia, thalassemia, autoimmune disease,
CC hemolytic or septic shock, hemophilia, inflammation and other stress
CC conditions, ischemia and other hypoxic conditions, carcinoma, leukemia,
CC Hodgkin disease, non-Hodgkin lymphoma and Kaposi sarcoma. It is also
CC useful for suppressing or eliminating infectious agents, autoimmune cells
CC and cancerous cells, and for preventing an infection or disease in a
CC patient. The present sequence represents an oligonucleotide containing
CC the hypoxia response enhancer (HRE) element from the human
CC phosphoglycerate kinase gene in the sense orientation. It is used
CC to produce vectors of the invention.
XX
XX Sequence 21 BP; 4 A; 7 C; 5 G; 5 T; 0 other:
SQ
Query Match 100.0%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCACTCTGCACGACGTA 21
DB 1 TGTCACTCTGCACGACGTA 21
RESULT 2
AAH42138
ID AAH42138 standard; DNA: 43 BP.
XX
XX AAH42138;
AC
XX
XX 17-SEP-2001 (first entry)
DT
XX
XX Synapsin gene 5' element and phosphoglycerate kinase gene HRE element.
KW Expression vector; silencer element; inducible element;
KW silencer-inducible region; gene therapy; cardiac disease;
KW immunodeficiency; allergy; anemia; thalassemia; autoimmune disease;
KW shock; hemophilia; inflammation; stress; ischemia; hypoxic condition;
KW carcinoma; leukemia; Hodgkin disease; Kaposi sarcoma; silencer element;
KW synapsin gene; hypoxia response enhancer; HRE;
KW phosphoglycerate kinase gene; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO200148187-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 15-DEC-2000; 2000WO-US33269.
PF
XX 23-DEC-1999; 99US-0171597.
PR
XX 28-NOV-2000; 2000US-0733326.
PR

PA (UWMI-) UNIV MIAMI.
XX
XX Webster KA.
PI
XX
XX WPI: 2001-441715/47.
DR
XX
XX Novel isolated expression vector useful therapeutically, comprises
PT silencer elements and conditionally inducible elements to form
PT silencer-inducible region, and a promoter in operative linkage with the
PT region -
XX
XX Disclosure: Page 25; 49pp; English.
XX
XX The specification describes an expression vector. The vector comprises
CC silencer elements and conditionally inducible elements to form a
CC silencer-inducible region (IR), and a promoter in operative linkage
CC with IR, where the promoter is regulated by IR, and upstream of the
CC expressed region. The vector is useful diagnostically, therapeutically,
CC prophylactically to make models of human disease. It is useful in gene
CC therapy, production of recombinant biologicals, genetic diagnosis, drug
CC screening, and genetic research (e.g., genomics, proteomics, in vivo
CC and in vitro models of human disease). It is useful for treating cardiac
CC disease (by reduction or prevention of ischemic damage, inhibition of
CC restenosis, neutralization of other pathological effects of heart or
CC vascular disease, or diagnosis of hypoxia), acquired or inherited
CC immunodeficiency, allergy, anemia, thalassemia, autoimmune disease,
CC hemolytic or septic shock, hemophilia, inflammation and other stress
CC conditions, ischemia and other hypoxic conditions, carcinoma, leukemia,
CC Hodgkin disease, non-Hodgkin lymphoma and Kaposi sarcoma. It is also
CC useful for suppressing or eliminating infectious agents, autoimmune cells
CC and cancerous cells, and for preventing an infection or disease in a
CC patient. The present sequence represents a construct comprising
CC a silencer (5' element) from the human synapsin gene and a hypoxia
CC response enhancer (HRE) element from the human phosphoglycerate kinase
CC gene. It is used to produce vectors of the invention.
XX
XX Sequence 43 BP; 8 A; 16 C; 11 G; 8 T; 0 other:
SQ
Query Match 100.0%; Score 21; DB 22; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCACTCTGCACGACGTA 21
DB 23 TGTCACTCTGCACGACGTA 43
RESULT 3
AAH42139
ID AAH42139 standard; DNA: 86 BP.
XX
XX AAH42139;
AC
XX
XX 17-SEP-2001 (first entry)
DT
XX
XX Synapsin gene 5' element and phosphoglycerate kinase gene HRE element.
KW Expression vector; silencer element; inducible element;
KW silencer-inducible region; gene therapy; cardiac disease;
KW immunodeficiency; allergy; anemia; thalassemia; autoimmune disease;
KW shock; hemophilia; inflammation; stress; ischemia; hypoxic condition;
KW carcinoma; leukemia; Hodgkin disease; Kaposi sarcoma; silencer element;
KW synapsin gene; hypoxia response enhancer; HRE;
KW phosphoglycerate kinase gene; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO200148187-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 15-DEC-2000; 2000WO-US33269.
PF

XX 23-DEC-1999; 990S-0171597.
PR 28-NOV-2000; 2000US-0723326.
XX
PA (UYM-) UNIV MIAMI.
XX Webster KA;
PI
XX WPI; 2001-441715/47.
DR
XX Novel isolated expression vector useful therapeutically, comprises
PT silencer elements and conditionally inducible elements to form
PT silencer-inducible region, and a promoter in operative linkage with the
PT region -
XX
PS Disclosure; Page 25; 49pp; English.
XX
CC The specification describes an expression vector. The vector comprises
CC silencer elements and conditionally inducible elements to form a
CC silencer-inducible region (IR), and a promoter in operative linkage
CC with IR, where the promoter is regulated by IR, and upstream of the
CC expressed region. The vector is useful diagnostically, therapeutically,
CC prophylactically to make models of human disease. It is useful in gene
CC therapy, production of recombinant biologicals, genetic diagnosis, drug
CC screening, and genetic research (e.g., genomics, proteomics, in vivo
CC and in vitro models of human disease). It is useful for treating cardiac
CC disease (by reduction or prevention of ischemic damage, inhibition of
CC restenosis, neutralization of other pathological effects of heart or
CC vascular disease, or diagnosis of hypoxia), acquired or inherited
CC immunodeficiency, allergy, anemia, thalassemia, autoimmune disease,
CC hemolytic or septic shock, hemophilia, inflammation and other stress
CC conditions, ischemia and other hypoxic conditions, carcinoma, leukemia,
CC Hodgkin disease, non-Hodgkin lymphoma and Kaposi sarcoma. It is also
CC useful for suppressing or eliminating infectious agents, autoimmune cells
CC and cancerous cells, and for preventing an infection or disease in a
CC patient. The present sequence represents a construct comprising
CC a silencer (SIL) element from the human synapsin gene and a hypoxia
CC response enhancer (HRE) element from the human phosphoglycerate kinase
CC gene. It is used to produce vectors of the invention.
XX
SQ Sequence 86 BP; 16 A; 32 C; 22 G; 16 T; 0 other;
Query Match 100.0%; Score 21; DB 22; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 TGTCAAGTCTCTGACGACGTA 21
|||||
23 TGTCAAGTCTCTGACGACGTA 43
RESULT 4
AAH42142
ID AAH42142 standard; DNA; 129 BP.
XX
AC AAH42142;
XX
DT 17-SEP-2001 (first entry)
XX
DE Synapsin gene SIL element and phosphoglycerate kinase gene HRE element.
XX
KW Expression vector; silencer element; inducible element;
KW silencer-inducible region; gene therapy; cardiac disease;
KW immunodeficiency; allergy; anemia; thalassemia; autoimmune disease;
KW shock; hemophilia; inflammation; stress; ischemia; hypoxic condition;
KW carcinoma; leukemia; Hodgkin disease; Kaposi sarcoma; silencer element;
KW synapsin gene; hypoxia response enhancer; HRE;
KW phosphoglycerate kinase gene; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200148187-A2.

XX 05-JUL-2001.
PD 15-DEC-2000; 2000WO-US333269.
XX
PF 23-DEC-1999; 990S-0171597.
XX 28-NOV-2000; 2000US-0723326.
PR
XX (UYM-) UNIV MIAMI.
PA Webster KA;
PI
XX WPI; 2001-441715/47.
DR
XX Novel isolated expression vector useful therapeutically, comprises
PT silencer elements and conditionally inducible elements to form
PT silencer-inducible region, and a promoter in operative linkage with the
PT region -
XX
PS Disclosure; Page 25; 49pp; English.
XX
CC The specification describes an expression vector. The vector comprises
CC silencer elements and conditionally inducible elements to form a
CC silencer-inducible region (IR), and a promoter in operative linkage
CC with IR, where the promoter is regulated by IR, and upstream of the
CC expressed region. The vector is useful diagnostically, therapeutically,
CC prophylactically to make models of human disease. It is useful in gene
CC therapy, production of recombinant biologicals, genetic diagnosis, drug
CC screening, and genetic research (e.g., genomics, proteomics, in vivo
CC and in vitro models of human disease). It is useful for treating cardiac
CC disease (by reduction or prevention of ischemic damage, inhibition of
CC restenosis, neutralization of other pathological effects of heart or
CC vascular disease, or diagnosis of hypoxia), acquired or inherited
CC immunodeficiency, allergy, anemia, thalassemia, autoimmune disease,
CC hemolytic or septic shock, hemophilia, inflammation and other stress
CC conditions, ischemia and other hypoxic conditions, carcinoma, leukemia,
CC Hodgkin disease, non-Hodgkin lymphoma and Kaposi sarcoma. It is also
CC useful for suppressing or eliminating infectious agents, autoimmune cells
CC and cancerous cells, and for preventing an infection or disease in a
CC patient. The present sequence represents a construct comprising
CC a silencer (SIL) element from the human synapsin gene and a hypoxia
CC response enhancer (HRE) element from the human phosphoglycerate kinase
CC gene. It is used to produce vectors of the invention.
XX
SQ Sequence 129 BP; 24 A; 48 C; 27 G; 30 T; 0 other;
Query Match 100.0%; Score 21; DB 22; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 TGTCAAGTCTCTGACGACGTA 21
|||||
23 TGTCAAGTCTCTGACGACGTA 43
RESULT 5
AAF85326/C
ID AAF85326 standard; DNA; 19 BP.
XX
AC AAF85326;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide fragment of plasmid pBS-HRE10.
XX
KW Nucleic acid construct; oxygen partial pressure; cellular hypoxia;
KW anemia; cancer; ischemia; erythropoietin; immunotherapy;
KW autoimmune disease; hH104; tTAK; ds.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200136616-A2.

PD 25-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-FR03207.
PF
XX
PR 18-NOV-1999; 99FR-0014513.
XX
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (AVET) AVENTIS PHARMA SA.
XX
XX Beuzard Y, Payen E, Scherman D, Beltan M;
DR WPI; 2001-343818/36.
XX
XX New nucleic acid construct for controlling expression of target gene,
PT useful e.g. for treating cancer, is modulated by exogenous
PT pharmaceutical and oxygen partial pressure
XX
XX
PS Disclosure; Page 18; 60pp; French.
XX
XX The specification describes a nucleic acid construct bearing a system
CC for regulating the expression of a gene. The nucleic acid construct
CC comprises at least one sequence encoding a protein that regulates
CC expression of at least one gene of interest. The activity of this
CC protein is modulated by presence/absence of a pharmacological agent
CC and the amount of protein produced depends on the oxygen partial
CC pressure. The constructs are used to treat conditions associated with
CC cellular hypoxia, especially anemia, cancer and ischemia, specifically
CC where the gene of interest encodes erythropoietin (but many other
CC suitable genes are listed, e.g. those encoding single-chain antibodies
CC for immunotherapy of infections or autoimmune diseases.
CC prodrug-converting enzymes, apoptosis inducers etc.). The present
CC sequence represents a fragment of PBS-HRE10, which was used to produce
CC constructs of the invention.
XX
SQ Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 other;
Query Match 90.5%; Score 19; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTACGTCCTGCACGACG 19
Db 19 TGTACGTCCTGCACGACG 19
RESULT 6
AA099458/c
ID AA099458 standard; DNA; 24 BP.
XX
XX AA099458;
XX
XX 19-MAR-1996 (first entry)
DE Hypoxia-inducible phosphoglycerate kinase-1 expression control sequence.
XX
XX Hypoxia; response element; erythropoietin; phosphoglycerate kinase;
KM PKR-1; gene therapy; tumour; cancer; P18; P24; ss.
XX
XX Mus sp.
OS
XX
XX W09521927-A2.
PN
XX
PD 17-AUG-1995.
XX
XX 15-FEB-1995; 95WO-GB00322.
PF
XX 15-FEB-1994; 94GB-0002857.
PR
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA
XX
XX Firth JD, Harris AL, Pugh CW, Ratcliffe PJ;
PI
XX
XX WPI; 1995-293128/38.

XX
XX Novel method of targeting gene therapy - using a hypoxically
PT inducible expression control sequence linked to a species active
PT against disease
XX
XX
PS Disclosure; Page 4; 30pp; English.
XX
XX AA099458 and AA099459 are hypoxia inducible transcription control
CC elements P24 and P18, respectively. P24 and P18 may be linked to at
CC least one gene encoding a protein that has activity against disease e.g.
CC CD2, CD4, etc. Such a construct may be used to treat a patient
CC suffering from a disease in which hypoxia is a cause or symptom.
CC The constructs are particularly used for treating tumours.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;
Query Match 90.5%; Score 19; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTACGTCCTGCACGACG 19
Db 21 TGTACGTCCTGCACGACG 3
RESULT 7
AA211422/c
ID AA211422 standard; DNA; 24 BP.
XX
XX AA211422;
AC
XX
DT 26-OCT-1999 (first entry)
XX
DE Hypoxia responsive sequence mPGK.
XX
XX Retroviral vector: functional splice donor site; hybrid viral vector;
KM functional splice acceptor site; in vivo gene delivery; therapeutic;
KM lentiviral vector; modified hematopoietic stem cell; MHC; tumour;
KM ischemia; hypoxia response element; HRE; hypoxia; ss.
XX
OS Mus sp.
XX
XX W09915684-A2.
PN
XX
PD 01-APR-1999.
XX
XX 23-SEP-1998; 98WO-GB02885.
PF
XX 25-SEP-1997; 97GB-0020465.
PR
XX 23-SEP-1997; 97GB-0020216.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
PA
XX
XX Bebbington C, Binley KM, Lewis C, Naylor S;
PI WPI; 1999-263482/22.
XX
XX New retroviral vectors, for, e.g. delivering nucleotide sequences to
PT solid tumor sites
PT
XX
XX
PS Example 1 (page 68); Fig 1 (page 1/43); 288pp; English.
XX
XX The invention relates to a retroviral vector (RVV) comprising a
CC functional splice donor site (FSDS) and a functional splice acceptor
CC site (FSAS) where: (i) the FSDS and the FSAS flank a first nucleotide
CC sequence of interest (NOI); (ii) the FSDS is upstream of the FSAS; (iii)
CC the RVV is derived from a retroviral pro-vector; (iv) the retroviral
CC pro-vector comprises a first nucleotide sequence (NS) capable of yielding
CC the FSDS and a second NS capable of yielding the FSAS; and (v) the first
CC NS is downstream of the second NS, such that the RVV is formed as a
CC result of reverse transcription of the retroviral pro-vector. A hybrid
CC viral vector (VV) system for in vivo gene delivery, which system
CC comprises a primary VV which encodes a secondary VV, the primary vector

OY 1 TGTACGTCCTGCACGACG 19
|||||
DB 21 TGTACGTCCTGCACGACG 3

RESULT 10
AAH42140
ID AAH42140 standard; DNA; 123 BP.

XX AAH42140;

XX 17-SEP-2001 (first entry)

DE Synapsin gene SIL element and phosphoglycerate kinase gene HRE element.

XX Expression vector; silencer element; inducible element;
KW silencer-inducible region; gene therapy; cardiac disease;
KW immunodeficiency; allergy; anemia; thalassemia; autoimmune disease;
KW shock; hemophilia; inflammation; stress; ischemia; hypoxic condition;
KW carcinoma; leukemia; Hodgkin disease; Kaposi sarcoma; silencer element;
KW synapsin gene; hypoxia response enhancer; HRE;
KW phosphoglycerate kinase gene; ss.

XX Synthetic.

XX Homo sapiens.

XX WO200148187-A2.

XX 05-JUL-2001.

XX 15-DEC-2000; 2000WO-US33269.

XX 23-DEC-1999; 99US-0171597.

XX 28-NOV-2000; 2000US-0723326.

XX (UWMT-) UNIV MIAMI.

XX Webster KA;

XX WPI; 2001-441715/47.

PT Novel isolated expression vector useful therapeutically, comprises a
PT silencer elements and conditionally inducible elements to form
PT silencer-inducible region, and a promoter in operative linkage with the
PT region -

PS Disclosure; Page 25; 49pp; English.

CC The specification describes an expression vector. The vector comprises
CC silencer elements and conditionally inducible elements to form a
CC silencer-inducible region (IR), and a promoter in operative linkage
CC with IR, where the promoter is regulated by IR, and upstream of the
CC expressed region. The vector is useful diagnostically, therapeutically,
CC prophylactically to make models of human disease. It is useful in gene
CC therapy, production of recombinant biologicals, genetic diagnosis, drug
CC screening, and genetic research (e.g., genomics, proteomics, in vivo
CC and in vitro models of human disease). It is useful for treating cardiac
CC disease (by reduction or prevention of ischemic damage, inhibition of
CC restenosis, neutralization of other pathological effects of heart or
CC vascular disease, or diagnosis of hypoxia), acquired or inherited
CC immunodeficiency, allergy, anemia, thalassemia, autoimmune disease,
CC hemolytic or septic shock, hemophilia, inflammation and other stress
CC conditions, ischemia and other hypoxic conditions, carcinoma, leukemia,
CC Hodgkin disease, non-Hodgkin lymphoma and Kaposi sarcoma. It is also
CC useful for suppressing or eliminating infectious agents, autoimmune cells
CC and cancerous cells, and for preventing an infection or disease in a
CC patient. The present sequence represents a construct comprising
CC a silencer (SIL) element from the human synapsin gene and a hypoxia
CC response enhancer (HRE) element from the human phosphoglycerate kinase
CC gene. It is used to produce vectors of the invention.

XX Sequence 123 BP; 22 A; 47 C; 32 G; 22 T; 0 other;

Query Match 90.5%; Score 19; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGTACGTCCTGCACGACG 19
|||||
DB 101 TGTACGTCCTGCACGACG 119

RESULT 11
AAZ11398/C

ID AAZ11398 standard; DNA; 229 BP.

XX AAZ11398;

XX 26-OCT-1999 (first entry)

DE PGK derived enhancer sequence in the context of MLV retroviral promoter.

XX Retroviral vector; functional splice donor site; hybrid viral vector;

XX functional splice acceptor site; in vivo gene delivery; therapeutic;

XX lentiviral vector; modified hematopoietic stem cell; MHSC; tumour;

XX ischemia; hypoxia response element; HRE; hypoxia; ss.

XX Synthetic.

XX Mus sp.

XX Murine leukemia virus.

XX WO9915684-A2.

XX 01-APR-1999.

XX 23-SEP-1998; 98WO-GB02885.

XX 25-SEP-1997; 97GB-0020465.

XX 23-SEP-1997; 97GB-0020216.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Bebbington C, Binley KM, Lewis C, Naylor S;

XX WPI; 1999-263482/22.

PT New retroviral vectors, for, e.g. delivering nucleotide sequences to
PT solid tumor sites

PS Example 1; Page 70; 288pp; English.

CC The invention relates to a retroviral vector (RVV) comprising a
CC functional splice donor site (FSDS) and a functional splice acceptor site
CC (FSAS) where: (i) the FSDS and the FSAS flank a first nucleotide sequence
CC of interest (NOI); (ii) the FSDS is upstream of the FSAS; (iii) the RVV
CC is derived from a retroviral pro-vector; (iv) the retroviral pro-vector
CC comprises a first nucleotide sequence (NS) capable of yielding the FSDS
CC and a second NS capable of yielding the FSAS; and (v) the first NS is
CC downstream of the second NS, such that the RVV is formed as a result of
CC reverse transcription of the retroviral pro-vector. A hybrid viral vector
CC (VV) system for in vivo gene delivery, which system comprises a primary
CC VV which encodes a secondary VV, the primary vector capable of infecting
CC a first target cell and of expressing the secondary VV, which secondary
CC vector is capable of transducing a secondary target cell, where the
CC primary vector is obtainable from or is based on an adenoviral vector and
CC the secondary VV is obtainable from or is based on a RVV preferably a
CC lentiviral vector (LVV) is also provided. The systems can be used for
CC delivering NOIs to one or more target sites. The NOIs may encode
CC therapeutic or diagnostic agents. The methods are used particularly for
CC producing modified hematopoietic stem cells (MHSCs) to deliver NOIs to
CC sites such as solid tumours which are characterised by ischemia, such as
CC hypoxia or low glucose concentration. The system permits the stable
CC expression of NOIs in targeted cells, e.g. rapidly dividing cells. The
CC present sequence represents a PGK derived enhancer sequence in the
CC context of MLV retroviral promoter, in the forward orientation.

SQ Sequence 229 BP; 52 A; 68 C; 55 G; 54 T; 0 other;
Query Match 90.5%; Score 19; DB 20; Length 229;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCAGCTCCTGCACGACG 19
|||||
DB 30 TGTCAGCTCCTGCACGACG 12
RESULT 12
AAH1996/c
ID AAH1996 standard; DNA; 229 BP.
XX
AC AAH1996;
14-AUG-2000 (first entry)
DE Murine PGK HRE derived enhancer DNA.
XX
KM HRE: hypoxia response element; hypoxia-inducible factor; HIF; vasotrophic;
KM cardiant; cytosstatic; antiarthritic; gene therapy; ischemia; arthritis;
KM cardiovascular disease; peripheral arterial disease; cancer;
KM phosphoglycerate kinase; PGK; murine; enhancer; ds.
XX
OS Mus sp.
XX WO200017371-A1.
XX 30-MAR-2000.
XX PD 22-SEP-1999; 99WO-GB03181.
XX PF 23-SEP-1998; 98WO-GB02885.
PR 28-JAN-1999; 99GB-0001906.
PR 16-FEB-1999; 99GB-0003538.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Blinley KM, Naylor S;
XX
DR WPI: 2000-283595/24.
XX
PT Novel polynucleotide constructs comprising at least two repeats of a
hypoxia response element useful for driving expression of nucleic acids
of interest in a cell under hypoxic conditions
XX
PS Example 3; Page 74-75; 155pp; English.
XX
CC This invention describes novel polynucleotide comprising at least 2
CC repeats of a hypoxia response element (HRE), where the hypoxia-inducible
CC factor (HIF) consensus binding sites within each of the 2 repeats are
CC separated by a spacer of at least 20 contiguous nucleotides. The products
CC of the invention have vasotrophic, cardiant, cytosstatic and antiarthritic
CC activity and can be used for gene therapy. The polynucleotides are useful
CC for delivering nucleic acids of interest to mammalian cells. Lentiviral
CC vectors are responsive to hypoxic agents and to agents that mimic
CC hypoxia. This regulation can be harnessed in vitro to enhance the
CC production of the vector and can be used in vivo to regulate gene
CC expression in response to a physiological signal. The vectors have
CC utility in disease, where ischemia, including hypoxia, is a feature,
CC e.g. cardiovascular disease, peripheral arterial disease, cancer and
CC arthritis. The novel regulatory construct is capable of driving very high
CC levels of transcription under conditions of hypoxia whilst providing only
CC low basal levels of transcription under normal oxygen conditions. The
CC polynucleotide construct targets cells within a tumor mass that are under
CC conditions of hypoxia without affecting normal surrounding tissue. This
CC sequence represents a murine phosphoglycerate kinase (PGK) HRE derived
CC enhancer which is described in the method of the invention.
XX
SQ Sequence 229 BP; 52 A; 68 C; 55 G; 54 T; 0 other;

Query Match 90.5%; Score 19; DB 21; Length 229;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCAGCTCCTGCACGACG 19
|||||
DB 30 TGTCAGCTCCTGCACGACG 12
RESULT 13
AAH20729/c
ID AAH20729 standard; DNA; 513 BP.
XX
AC AAH20729;
XX
DT 13-AUG-2001 (first entry)
XX
DE Murine phosphoglycerate kinase promoter DNA.
XX
KM Phosphoglycerate kinase; promoter; gene therapy; amniocyte; cytosstatic;
KM E1A region; E1B region; modified tropism; tumor; ds.
XX
OS Mus sp.
XX WO200136615-A2.
XX
PD 25-MAY-2001.
XX
PF 07-NOV-2000; 2000WO-EP10992.
XX
PR 18-NOV-1999; 99DE-1055558.
XX
PA (KOCH/) KOCHANER S.
XX
PI Kochanek S, Schiedner G;
XX
DR WPI: 2001-343817/36.
XX
PT New permanent amniocyte cell lines, useful for producing viral gene
PT therapy vectors or mutant adenoviruses, express the adenoviral E1A and
PT E1B gene products -
XX
PS Example 1; Page 61; 72pp; German.
XX
CC This invention describes novel permanent amniocyte cell lines (A),
CC containing at least one nucleic acid (1) that causes expression of the
CC gene products (11) of the adenoviral E1A and E1B regions. (A) are used to
CC produce gene therapy vectors, especially adeno, adeno-associated, retro
CC or lentiviral vectors, particularly first- or second generation,
CC large-capacity or deleted adenoviral vectors. (A) are also used to
CC produce adenoviral mutants, optionally with modified tropism. The vectors
CC may express a wide range of therapeutic proteins or antisense RNAs.
CC Adenoviral mutants, unable to express the E1B 55 kDa protein, are useful
CC for treating tumors, they replicate in the cells but not significantly in
CC normal primary cells. (A) can be made efficiently, simply and
CC reproducibly. The products of the invention have cytosstatic activity.
CC This sequence represents the murine phosphoglycerate kinase promoter
CC found in plasmid SK146.
XX
SQ Sequence 513 BP; 79 A; 171 C; 161 G; 102 T; 0 other;
Query Match 90.5%; Score 19; DB 22; Length 513;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCAGCTCCTGCACGACG 19
|||||
DB 235 TGTCAGCTCCTGCACGACG 217
RESULT 14
AAS05243/c
ID AAS05243 standard; DNA; 4768 BP.

XX AAS05243;
AC
XX
DT 07-SEP-2001 (first entry)
XX-
DE Plasmid vector pDG2 used as a construct for TRP genes.
XX
XX Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; pDG2;
KM transgenic animal; knockout mouse; triplet repeat expansion;
KM fragile X syndrome; Huntington's disease; cyclic; circular; ds.
XX
OS Synthetic.
XX
PN WO200130798-A1.
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000MO-US29382.
XX
PR 26-OCT-1999; 99US-0161488.
XX
PA (DELT-) DELTAGEN INC.
DR Klein R, Matthews W, Moore M, Allen KD;
XX WPI; 2001-300473/31.
PT Novel transgenic animals useful as animal model for characterization of
PT function of a gene encoding trinucleotide repeat proteins (TRPs),
XX contains heterozygous disruption in a gene encoding TRP -
XX
XX Disclosure; Fig 2B; 106pp; English.
XX
CC The present sequence for plasmid vector pDG2 is used as a construct
CC for genes encoding trinucleotide repeat proteins (TRP) such as gene
CC T243 to produce disruption in the DNA. The invention describes
CC methods of producing embryonic stem (ES) cells comprising a heterozygous
CC disruption in a target DNA sequence (preferably T243) encoding a TRP and
CC of producing a knockout mouse comprising a homozygous disruption in a
CC gene encoding TRP, where the disruption inhibits the production of the
CC wild type TRP. The invention also relates to identifying agents capable
CC of affecting a phenotype of a knockout mouse. Also described are methods
CC of determining whether expansion of the trinucleotide repeat in a gene
CC encoding TRP produces a phenotypic change. The transgenic animals and
CC the cells are useful for identifying compounds capable of ameliorating
CC disease symptoms, and as test substrates for the identification of drugs,
CC pharmaceuticals, therapies and interventions which may be effective in
CC treating trinucleotide repeat disorders e.g. fragile X syndrome and
CC Huntington's disease. The animal models for trinucleotide repeat
CC disorders are ideal model systems to study the progression of disease in
CC vivo, the molecular basis of these diseases and show the features
CC observed in human disease. Using the mice, it is possible to model both
CC the pathogenic mechanism and the trinucleotide repeat instability in the
CC mouse.
XX
SQ Sequence 4768 BP; 1124 A; 1218 C; 1269 G; 1157 T; 0 other;
XX
XX
Query Match 90.5%; Score 19; DB 22; Length 4768;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTACAGTCTCTGCACGACG 19
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 2838 TGTACAGTCTCTGCACGACG 2820
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 15
ABLA2019/C
ID ABLA2019 standard; DNA: 4768 BP.
AC ABLA2019;
XX
XX 11-JUN-2002 (first entry)

XX Nucleotide sequence of vector pDG2.
DE
XX
XX pDG2; transgenic animal; matrix metalloproteinase-23 gene; MMP-23 gene;
KM ss.
XX
XX Synthetic.
OS
XX
PN US2002023275-A1.
PD 21-FEB-2002.
XX
PF 17-MAY-2001; 2001US-0861077.
XX
PR 17-MAY-2000; 2000US-204972P.
PR 29-JUN-2000; 2000US-215394P.
XX
PA (LEVI/) LEVITEN M W.
XX
PI Leviten MW;
XX
DR WPI; 2002-255684/30.
XX
PT Non-human transgenic animal useful as a model for disease and for
PT identifying agents that modulate gene expression and gene function,
XX comprises a disruption in the matrix metalloproteinase-23 gene -
XX
XX Example 1; Fig 2B; 38pp; English.
XX
XX The present sequence represents vector pDG2. This vector contains an
XX ampicillin resistance gene and a neomycin gene. The vector is used in
XX the invention. The specification describes a non-human transgenic animal
XX comprising a disruption in the matrix metalloproteinase (MMP)-23 gene.
XX Transgenic animals of the invention comprising a homozygous or
XX heterozygous disruption in MMP23 gene are useful for identifying agents
XX which modulate MMP23 expression or function. They are also useful for
XX identifying agents that are capable of ameliorating a phenotype of a
XX transgenic animal comprising a disruption in an MMP-23 gene or
XX ameliorating a disease associated with the phenotype of a transgenic
XX animal comprising a disruption in the MMP-23 gene. The animals are
XX useful as an animal model for diseases, disorders and conditions
XX characterized by a disruption in a gene encoding a metalloproteinase,
XX more particularly disease, disorders and conditions associated with the
XX phenotypes demonstrated by the knockout mice. The transgenic animals
XX are useful as test substrates for identification of drugs,
XX pharmaceuticals and therapies effective in treating diseases, disorders
XX and conditions associated with disruption in the target gene. The
XX animal is useful for testing and developing new treatments relating
XX to behavioural phenotypes demonstrated by the animal models.
XX
SQ Sequence 4768 BP; 1124 A; 1218 C; 1269 G; 1157 T; 0 other;
XX
XX
Query Match 90.5%; Score 19; DB 24; Length 4768;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTACAGTCTCTGCACGACG 19
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
DB 2838 TGTACAGTCTCTGCACGACG 2820
XXXXXXXXXXXXXXXXXXXXXXXXXXXX
Search completed: July 9, 2003, 14:21:43
Job time: 147 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 9, 2003, 09:54:55 ; Search time 1136 seconds
(without alignments)
299.388 Million cell updates/sec

Title: US-09-723-326B-1
Perfect score: 21
Sequence: 1 tgcacgtcctgcacgcacgta 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Archived: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbda:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_huv:*
20: em_gss_pln:*
21: em_gss_vrl:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	81.0	553	17	BH887440 LB01441a.
2	17	81.0	631	17	BH888010 LB01794a.
3	16.8	80.0	395	12	BG286598 602381606
4	16.8	80.0	594	14	BQ664135 HV02A03u
5	16.8	80.0	927	10	BE290997 601084169
6	16.8	80.0	1098	17	CNS0674V ALA14101 17 end of

C	7	16.8	80.0	1574	17	A2133021	A2133021	OSJNB010
C	8	16.4	78.1	307	17	A2578287	A2578287	21b03 Shc
C	9	16.4	78.1	383	12	BF743507	BF743507	OYO -BT080
C	10	16.4	78.1	419	13	BM322991	BM322991	PTC1_11_B
C	11	16.4	78.1	615	17	AO397741	AO397741	m9xb00171
C	12	16.2	77.1	197	17	BH049064	BH049064	RPCI -24-2
C	13	16.2	77.1	343	12	BE836447	BE836447	PM2 -FN006
C	14	16.2	77.1	544	17	AO078346	AO078346	CIT -HSP-2
C	15	16.2	77.1	622	17	BH141668	BH141668	TDGDC37TH
C	16	16.2	77.1	661	17	AG136658	AG136658	Pan trogl
C	17	16.2	77.1	690	13	BI151875	BI151875	602916373
C	18	16.2	77.1	920	17	CNS029RX	AL187624	Tetraodon
C	19	16.2	77.1	930	17	CNS04EK8	AL287153	Tetraodon
C	20	16.2	77.1	1123	14	BO712663	AL248672	ACENICOURT
C	21	16.2	77.1	1126	17	CNS03KYB	AL248672	Tetraodon
C	22	16.2	77.1	1635	12	BG483774	BG483774	602503419
C	23	16.2	77.1	1874	10	AW729726	AW729726	Ga_Ea002
C	24	16.2	77.1	404	17	AO113596	AO113596	CIT -HSP-2
C	25	15.8	75.2	186	12	BG188939	BG188939	RST97974 A
C	26	15.8	75.2	197	12	BG190578	BG190578	RST9651 A
C	27	15.8	75.2	199	12	BG197706	BG197706	RST16935
C	28	15.8	75.2	219	12	BG185274	BG185274	RST4213 A
C	29	15.8	75.2	220	12	BG212794	BG212794	RST32389
C	30	15.8	75.2	221	12	BG192598	BG192598	RST9114 A
C	31	15.8	75.2	226	12	BG190058	BG190058	RST9114 A
C	32	15.8	75.2	231	12	BG198722	BG198722	RST17991
C	33	15.8	75.2	236	12	BG203387	BG203387	RST22768
C	34	15.8	75.2	288	14	BM965404	BM965404	KJ95d12.Y
C	35	15.8	75.2	431	17	BH753428	BH753428	SALK_0288
C	36	15.8	75.2	454	10	AV619431	AV619431	AV619431
C	37	15.8	75.2	466	9	AJ280880	AJ280880	AA3A-AAV-
C	38	15.8	75.2	467	9	AL587460	AL587460	AL587460
C	39	15.8	75.2	482	12	BF625474	BF625474	HYSMA000
C	40	15.8	75.2	498	10	AM592678	AM592678	h46a04.x
C	41	15.8	75.2	520	13	BI776024	BI776024	468768 MA
C	42	15.8	75.2	571	17	LI091AY	AL354057	Leishmani
C	43	15.8	75.2	588	14	BU005199	BU005199	OGG7614.Y
C	44	15.8	75.2	604	13	BM340142	BM340142	MEST319-A
C	45	15.8	75.2	608	14	BQ483290	BQ483290	WHE3506_G

ALIGNMENTS

RESULT 1
LOCUS BH887440/c 553 bp DNA linear GSS 07-AUG-2002
DEFINITION LB01441a.d.sp6.1 Leishmania major Friedlin BAC Library Leishmania
ACCESSION BH887440 major genomic clone LB01441a, DNA sequence.
VERSION BH887440.1 GI:22132375
KEYWORDS GSS.
SOURCE Leishmania major.
ORGANISM Leishmania major.
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
REFERENCE 1 (bases 1 to 553)
AUTHORS Myler,P.J., Vogt,C., Munden,H., Robertson,L., Sisk,E., Pazellina,G., Aggarwal,G., Nelson,S., Seyler,A., Worthley,E., Stuart,K. and Ragland,M.
TITLE Leishmania major Friedlin BAC End Sequences
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: LB01441a.d.T7.1
Contact: Myler PJ
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-0313
Email: mylerpj@sbri.org
Seq primer: Sp6
Class: BAC ends.
FEATURES
location/Qualifiers
1..553
source

```

/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone_lib="LB01441a"
/clone_lib="Leishmania major Friedlin BAC Library"
/clone_lib="E. coli GeneHogs + TrifA"
/Note="Vector: pCG270; Site: 1: HindIII; Genomic DNA from
Leishmania major Friedlin in agarose blocks was partially
digested with HindIII, size selected, and ligated with
HindIII-digested pCG270 vector DNA. 10368 clones were
picked and arrayed in 384- and 96-well plates. Library
construction and arraying was carried out by ResGen
Corporation and clones and filters are available from
them"

BASE COUNT      89 a      175 c      191 g      98 t
ORIGIN

Query Match      81.0%; Score 17; DB 17; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 CACGCTCTGCAGCAGCT 20
|||||
427 CACGCTCTGCAGCAGCT 411

RESULT 2
BH888010/c      631 bp      DNA      linear      GSS 07-AUG-2002
LB01794a.d.T7.1 Leishmania major Friedlin BAC Library Leishmania
DEFINITION
major genomic clone LB01794a, DNA sequence.
ACCESSION
BH888010
VERSION
BH888010.1 GI:22133715
KEYWORDS
GSS.
SOURCE
Leishmania major.
ORGANISM
Leishmania major.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
1 (bases 1 to 631)
Myler, P.J., Vogt, C., Munden, H., Robertson, L., Sisk, E., Fazelinia, G.,
Aggarwal, G., Nelson, S., Seyler, A., Worthey, E., Stuart, K. and
Rayland, M.
Leishmania major Friedlin BAC End Sequences
Unpublished (2002)
Other GSSs: LB01794a.d.SP6.1
Contact: Myler PJ
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-0313
Email: mylerpj@sbri.org
Seq primer: 17
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..631
/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone_lib="LB01794a"
/clone_lib="Leishmania major Friedlin BAC Library"
/clone_lib="E. coli GeneHogs + TrifA"
/Note="Vector: pCG270; Site: 1: HindIII; Genomic DNA from
Leishmania major Friedlin in agarose blocks was partially
digested with HindIII, size selected, and ligated with
HindIII-digested pCG270 vector DNA. 10368 clones were
picked and arrayed in 384- and 96-well plates. Library
construction and arraying was carried out by ResGen
Corporation and clones and filters are available from
them"

BASE COUNT      104 a      189 c      224 g      114 t
ORIGIN

Query Match      81.0%; Score 17; DB 17; Length 631;

```

```

Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 CACGCTCTGCAGCAGCT 20
|||||
428 CACGCTCTGCAGCAGCT 412

RESULT 3
BG286598
LOCUS
BG286598
DEFINITION
BG286598
602381606f1 NIH_MGC_93 Homo sapiens CDNA clone IMAGE:4499448 5',
mRNA sequence.
ACCESSION
BG286598
VERSION
BG286598.1 GI:13039617
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 395)
NIH-MGC http://img.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA library Preparation: Life Technologies, Inc.
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10363 row: k column: 01
High quality sequence stop: 388.

FEATURES
source
Location/Qualifiers
1..395
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4499448"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/Note="Organ: bladder; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: This is a NIH_MGC library."

BASE COUNT      85 a      97 c      117 g      96 t
ORIGIN

Query Match      80.0%; Score 16.8; DB 12; Length 395;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 GTCACGCTCTGCAGCAGTA 21
|||||
248 GTCACGCTCTGCAGCAGTA 267

RESULT 4
B0664135
LOCUS
B0664135
DEFINITION
B0664135
594 bp      mRNA      linear      EST 15-JUL-2002
HV02A03u HV Hordeum vulgare cDNA clone HV02A03 3-PRIME, mRNA
sequence.
ACCESSION
B0664135
VERSION
B0664135.1 GI:21805268
KEYWORDS
EST.
SOURCE
Hordeum vulgare.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
Triticeae; Hordeum.

```

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 594)	Zhang, H., Potokina, E., Michalek, W., Weschke, W., Stein, N. and Graner, A.	Barley Esns from germinating seeds	Unpublished (2002)	Contact: Stein Nils

Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 594 Std Error: 0.00
Plate: 2 row: A column: 3
Seq primer: MJ3un1.

FEATURES	Location/Qualifiers
source	1..594

```

source
1. .594
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="GABI:147814"
/db_xref="taxon:4513"
/clone="HV02A03"
/clone_1db="HV"
/tissue_type="germinating seeds"
/dev_stage="germinating seeds (48-96 h)"
/lab_host="XL10-Gold"
/note="Vector: pBluescript SK+, Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA): Roots were grown for two days on filter paper at room temperature. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter * used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/White selection for recombinants is not 100% reliable. Average insert size is 1 kb"
89 a      242 c      172 g      91 t
BASE COUNT
        1
origin

```

Query Match	80.0%	Score 16.8	DB 14	Length 594
Best Local Similarity	90.0%	Pred. No. 1.7e+03		
Matches 18	Conservative 0	Mismatches 2	Indels 0	Gaps 0
1	TGTCACGTCCTGCACGACGT	20		
284	TGTACGCTCCGGCAGCAGCT	303		

RESULT 5	BE290997	LOCUS	DEFINITION
BE290997	927 bp	mRNA	EST 13-JUL-2000
60108416	NCI_CGAP_Mam6	Mus musculus	CDNA clone IMAGE:3498353 5'
mRNA sequence_			

ACCESSION	BE290997
VERSION	BE290997.1
KEYWORDS	GI:9172417
SOURCE	EST.
ORGANISM	house mouse.
	Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nhl.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus
1 (bases 1 to 927)

Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINTL at: <http://image.llnl.gov>

```

Plate: L1M8553  row: j  column: 18
High quality sequence start: 3
High quality sequence stop: 35.
Location/Qualifiers
1. 927
FEATURES
SOURCE
```

```

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="3498353"
/clone_id="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

```

	Query Match	80.0%;	Score 16.8;	DB 10;	Length 927;
	Best Local Similarity	90.0%;	Pred. No.1.9e+03;		
Matches	18; Conservative	0;	Mismatches	2;	Indels
Gaps				0;	
OY	TGTCAGCTCCGCACGACT	20			
Dg	18 TGTCAGCTGTGCACGCCGT	37			

RESULT 6	CNS0674V	1098 bp	DNA	linear	GSS 05-JUL-2001
LOCUS	CNS0674V				
DEFINITION	T7 end of clone AW0A028H07 of library AW0A from strain CLB 89 of Yarrowia lipolytica, genomic survey sequence.				
ACCESSION	AL414101				
VERSION	AL414101.1	GI:12186881			
KEYWORDS	GSS.				
SOURCE	Yarrowia lipolytica.				
ORGANISM	Yarrowia lipolytica				

REFERENCE
1 (bases 1 to 1098)
Souchet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
AUTHORS

TITLE
Genomic exploration of the hemiascomycetous yeasts: I. A set of yeast species for molecular evolution studies
JOURNAL
FEBS Lett. 487 (1), 3-12 (2000)

REFERENCE 2 (bases 1 to 1098)

AUTHORS Casaregola, S., Neugeilise, C., Leplinge, A., Bon, E., Feynerol, C., Artiguenave, F., Wincker, P. and Galliard, C.

TITLE Genomic exploration of the hemiascomycetous yeasts: 17. *Yarrowia lipolytica*

JOURNAL
FEBs Lett. 48/ (1), 95-100 (2000)
MEDLINE 20584727
PUBMED 11152892
REFERENCE 3 (bases 1 to 1098)
SEQUENCE 3

TITLE Direct Submission
JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
sqgrate@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen

yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Phibia*

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

Source

Location/Qualifiers
1..1098
/organism="Yarrowia lipolytica"
/strain="CLIB 89"
/db_xref="taxon:4952"
/clone="AM0A028H07"
/clone_1lb="AM0A"
/note="end : 17"

BASE COUNT 279 a 290 c 257 g 268 t 4 others

ORIGIN

Query Match 80.0%; Score 16.8; DB 17; Length 1098;
Best Local Similarity 90.0%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY

1 TGTCAGTCTGCACGACGT 20
|||||
913 TGTCAGTCTGCACGACGT 932

RESULT 7 1574 bp DNA linear GSS 02-JUN-2000
A2133021/c 1574 bp DNA linear GSS 02-JUN-2000

LOCUS OSJNB0108124f CUGI Rice BAC library (ECORI) Oryza sativa genomic

DEFINITION clone OSJNB0108124f, DNA sequence.

ACCESSION A2133021 GI:8211768

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa.
Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzaeae; Oryza.
1 (bases 1 to 1574)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Seq primer: GTAAACGACGCGCCAGTG
Class: BAC ends

High quality sequence stop: 1574.

Location/Qualifiers

FEATURES

Source

1..1574
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="OSJNB0108124f"
/clone_1lb="CUGI Rice BAC library (ECORI)"
/tissue="leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBACindigo; site_1: EORI; site_2: EORI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumunathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping, and genome sequencing of rice,

we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu).

BASE COUNT 381 a 399 c 323 g 466 t 5 others

ORIGIN

Query Match 80.0%; Score 16.8; DB 17; Length 1574;
Best Local Similarity 90.0%; Pred. No. 2.3e+03; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY

2 GTCAGTCTGCACGACGTA 21
|||||
739 GTCAGTCTGCACGACGTA 720

RESULT 8

LOCUS

A2578287/c 307 bp DNA linear GSS 08-DEC-2000

DEFINITION 21b03 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium

sp. NGR234 genomic clone 21b03, DNA sequence.

ACCESSION A2578287 GI:11605415

VERSION

KEYWORDS

SOURCE

ORGANISM

Rhizobium sp. NGR234.
Rhizobium sp. NGR234
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
1 (bases 1 to 307)
Viprey, V., Rosenthal, A., Broughton, W.J. and Perret, X.
Genetic snapshots of the Rhizobium species NGR234 genome
Genome Biol. 1 (6), RESEARCH0014 (2000)

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

Contact: Virginie Viprey
Laboratoire de Biologie Moléculaire des Plantes Supérieures
University of Geneva
1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerland
Tel: +44(0)1603450000
Fax: +44(0)1603450045
Email: virginie.viprey@bsrc.ac.uk

COMMENT

Class:

shotgun.

Location/Qualifiers

1..307
/organism="Rhizobium sp. NGR234"
/strain="ANU265"
/db_xref="taxon:394"
/clone="21b03"
/clone_1lb="Shot-gun genomic library of Rhizobium strain
ANU265"
/note="Vector: M13; derivative strain of NGR234 cured of
pNGR234a"

BASE COUNT

64 a 93 c 90 g 60 t

ORIGIN

Query Match 78.1%; Score 16.4; DB 17; Length 307;
Best Local Similarity 94.4%; Pred. No. 2.2e+03; 2; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY

3 TCAGTCTGCACGACGT 20
|||||
199 TCAGTCTGCACGACGT 182

RESULT 9

LOCUS

BF743507/c 383 bp mRNA linear EST 10-JAN-2001

DEFINITION

QVO-BT0846-121000-434-e09 BT0846 Homo sapiens cDNA, mRNA sequence.

TITLE	Sudman, M. and Pratt, L. H.			
JOURNAL	An EST database from Sorghum: plants infected with a compatible pathogen			
COMMENT	Unpublished (2002) Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu			
FEATURES	Sequences have been trimmed to exclude POLYA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyMTMx or T7 sequencing primer, are presented as the reverse complement. Seq primer: JEN REV High quality sequence stop: 413 POLYA-No.			
SOURCE	Location/Qualifiers			
	1. 419			
	/organism="Sorghum bicolor"			
	/cultivar="BRx623"			
	/db_xref="taxon:4558"			
	/clone_id="Pathogen-infected compatible 1 (P1C1)"			
	/rname_type="leaves"			
	/dev_stage="4-week-old seedlings infected with Colletotrichum graminicola"			
	/note="Vector: plasmidscript II SK(-) from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; Four-week-old sorghum seedlings were sprayed with spore suspension prepared from 3-week-old FRM421, a sorghum isolate of the anthracnose pathogen Colletotrichum graminicola. Inoculated plants were kept in a 25 C dark growth chamber with 100% relative humidity for 24 hr, followed by 12/12 hr of light/dark cycle at 25 C with 90% relative humidity for another 24 hr. All leaves were harvested and quick frozen with liquid nitrogen and stored in a -80 C freezer. The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."			
BASE COUNT	73 a	146 c	110 g	90 t
ORIGIN				
Query Match	78.1%;	Score 16.4;	DB 13;	Length 419;
Best Local Similarity	94.4%;	Pred. No. 2.3e+03;		
Matches 17; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
OY	2	GTCACGCTCGACGACG 19		
Db	237	GTCACGCTCGACGACG 254		
RESULT 11				
LOCUS	AO397741	615 bp	DNA	GSS 06-MAR-1999
DEFINITION	mxb00017111f CUGI Rice Blast BAC library Magnaporthe grisea genomic clone mxb00017111f, DNA sequence.			
ACCESSION	AO397741			
VERSION	AO397741.1	GI:4368768		
KEYWORDS	GSS.			
SOURCE	Magnaporthe grisea.			
ORGANISM	Magnaporthe grisea			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 615)			
AUTHORS	Yu, Y., Zhu, H., Boyd, C. A., Gandette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wing, R. A. and Dean, R. A.			
TITLE	A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome			
JOURNAL	Unpublished (1998)			
COMMENT	Contact: Dean RA			

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdeane@clemson.edu
Seq primer: TAAATACGATCCTACATATAGCG
Class: BAC ends
High quality sequence stop: 216.

FEATURES

Source

Location/Qualifiers
1. 615
/organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0017111f"
/clone_lib="CUGI Rice Blast BAC Library"
/rissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25x genome coverage. High density colony filters
are available upon request."

BASE COUNT

97 a 244 c 140 g 134 t

ORIGIN

Query Match 78.1%; Score 16.4; DB 17; Length 615;
Best Local Similarity 94.4%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TGTACGTCCTGCACGAC 18
|||||
Db 332 TGTACGTCCTGCACGAC 349

RESULT 12
BH049064/c 197 bp DNA linear GSS 17-JUL-2001
LOCUS BH049064
DEFINITION RPI-24-232K18.TJ RPI-24 Mus musculus genomic clone RPI-24-232K18
, DNA sequence.
ACCESSION BH049064
KEYWORDS BH049064.1 GI:14837619
SOURCE GSS.
ORGANISM house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 197)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akintet, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shwartsbeyn, A., Gebregorgis, E.,
Russell, D., de Jong, P. and Fraser, C. M.
Mouse BAC End Sequences from Library RPI-24
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaot@igrr.org
Clones are derived from the mouse BAC library RPI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@igrr.org). Clones may be purchased from BACPAC
Resources (<http://www.chori.org/bacpac/orderframe.htm>). BAC end
page: http://www.tigr.org/tftp/bac-ends/mouse/bac_end_intro.html
Plate: 232 row: K column: 18
Seq primer: SP6

FEATURES

Source

Class: BAC ends.
Location/Qualifiers
1. 197
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPI-24-232K18"
/clone_lib="RPI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamHI; Site_2: BamHI;
RPI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

BASE COUNT 70 a 32 c 56 g 39 t

ORIGIN

Query Match 77.1%; Score 16.2; DB 17; Length 197;
Best Local Similarity 85.7%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TGTACGTCCTGCACGACGTA 21
|||||
Db 146 TGTACGTCCTGCACAGGTA 126

RESULT 13
BE836447/c 343 bp mRNA linear EST 22-SEP-2000
LOCUS BE836447
DEFINITION PM2-FN0061-280600-002-B03 FN0061 Homo sapiens CDNA, mRNA sequence.
ACCESSION BE836447
VERSION BE836447.1 GI:10268825
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 343)
Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=6t2-PM2-FN0061-280>)
600-002-B036t3=2000-06-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 57
High quality sequence stop: 342.
Location/Qualifiers
1. 343
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0061"
/dev_stage="Adult"
/note="Organ: prostate, normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent

FEATURES

Source

1. 343
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0061"
/dev_stage="Adult"
/note="Organ: prostate, normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 104 a 73 c 87 g 79 t

Query Match 77.1%; Score 16.2; DB 12; Length 343;
Best Local Similarity 85.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTACGCTCTGCACGAGTA 21
|||||
195 TGTACGCTCTGCACGAGTA 175

RESULT 14
078346 544 bp DNA linear GSS 20-AUG-1998

DEFINITION CIT-HSP-2363K18.TF CIT-HSP Homo sapiens genomic clone 2363K18, DNA sequence.

ACCESSION A0078346
VERSION A0078346
KEYWORDS GSS.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 544)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)

Other-GSS: CIT-HSP-2363K18.TR
Contact: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21

Class: BAC ends.
Location/Qualifiers

FEATURES
source 1..544
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2363K18"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; site_1: HindIII; site_2: HindIII"

BASE COUNT 155 a 107 c 123 g 159 t

Query Match 77.1%; Score 16.2; DB 17; Length 544;
Best Local Similarity 85.7%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTACGCTCTGCACGAGTA 21
|||||
434 TGTACGCTCTGCACGAGTA 454

RESULT 15
BH141668 622 bp DNA linear GSS 16-AUG-2001
LOCUS BH141668

DEFINITION TDGDG37TH cT0G Lycopersicon esculentum genomic clone cT0G2261, DNA sequence.
ACCESSION BH141668
VERSION BH141668.1 GI:15193897
KEYWORDS GSS.
SOURCE Tomato.

Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Solanales; Solanaceae; Solanum;

Lycopersicon.
1 (bases 1 to 622)

van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and Tanksley,S.

Tomato Demethylated Genomic DNA Sequences
Unpublished (2001)

COMMENT

Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA

Email: http://www.genome.clemson.edu/orders/index.html
tomato demethylated genomic DNA

Insert Length: 1270 Std Error: 0.00
Seq primer: M13F-R
Class: Shotgun.

FEATURES
source 1..622
Location/Qualifiers

/organism="Lycopersicon esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cT0G2261"
/clone_lib="cT0G"
/tissue_type="Young leaves"
/dev_stage="12-14 weeks post harvest"
/lab_host="E.coli JM109"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library was made from short EcoRI digested fragments of the genome of Lycopersicon esculentum ligated into pBS (SK-). The fragments were cloned into the methylation restrictive E.coli strain JM109 with the purpose of enriching the library for non-methylated DNA fragments. This procedure may enrich the pool of cloned fragments in JM109 cells for sequences representing expressed genes. Average insert size 1.27 kb."

BASE COUNT 154 a 170 c 127 g 171 t

Query Match 77.1%; Score 16.2; DB 17; Length 622;
Best Local Similarity 85.7%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTACGCTCTGCACGAGTA 21
|||||
DB 409 TGTACGCTCTGCACGAGTA 429

Search completed: July 9, 2003, 14:40:54
Job time: 1141 secs

THIS PAGE BLANK (USPTO)